

-1-

SEQUENCE LISTING

<110> Beamer, Lesa J.
Eisenberg, David
Carroll, Stephen F.

<120> BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN:
CRYSTALLIZATION, X-RAY DIFFRACTION, THREE-DIMENSIONAL
STRUCTURE DETERMINATION, RATIONAL DRUG DESIGN AND
MOLECULAR MODELING OF RELATED PROTEINS

<130> 11034US02

<140> 09/446,415

<141> 2000-07-19

<150> 08/879,565

<151> 1997-06-20

<160> 14

<170> PatentIn Ver. 2.1

<210> 1

<211> 1813

<212> DNA

<213> Human

<220>

<221> CDS

<222> (31)..(1491)

<220>

<221> mat_peptide

<222> (124)..(1491)

<220>

<223> "rBPI"

<400> 1

caggccttga gggttttggca gctctggagg atg aga gag aac atg gcc agg ggc 54
Met Arg Glu Asn Met Ala Arg Gly
-30 -25

cct tgc aac gcg ccg aga tgg gtg tcc ctg atg gtg ctc gtc gcc ata 102
Pro Cys Asn Ala Pro Arg Trp Val Ser Leu Met Val Leu Val Ala Ile
-20 -15 -10

ggc acc gcc gtg aca gcg gcc gtc aac cct ggc gtc gtg gtc agg atc 150
Gly Thr Ala Val Thr Ala Ala Val Asn Pro Gly Val Val Val Arg Ile
-5 -1 1 5

tcc cag aag gcc ctg gac tac gcc agc cag cag ggg acg gcc gct ctg 198
Ser Gln Lys Gly Leu Asp Tyr Ala Ser Gln Gln Gly Thr Ala Ala Leu
10 15 20 25

cag aag gag ctg aag agg atc aag att cct gac tac tca gac agc ttt 246

-2-

Gln Lys Glu Leu Lys Arg Ile Lys Ile Pro Asp Tyr Ser Asp Ser Phe	
30 35 40	
aag atc aag cat ctt ggg aag ggg cat tat agc ttc tac agc atg gac	294
Lys Ile Lys His Leu Gly Lys Gly His Tyr Ser Phe Tyr Ser Met Asp	
45 50 55	
atc cgt gaa ttc cag ctt ccc agt tcc cag ata agc atg gtg ccc aat	342
Ile Arg Glu Phe Gln Leu Pro Ser Ser Gln Ile Ser Met Val Pro Asn	
60 65 70	
gtg ggc ctt aag ttc tcc atc agc aac gcc aat atc aag atc agc ggg	390
Val Gly Leu Lys Phe Ser Ile Ser Asn Ala Asn Ile Lys Ile Ser Gly	
75 80 85	
aaa tgg aag gca caa aag aga ttc tta aaa atg agc ggc aat ttt gac	438
Lys Trp Lys Ala Gln Lys Arg Phe Leu Lys Met Ser Gly Asn Phe Asp	
90 95 100 105	
ctg agc ata gaa ggc atg tcc att tcc gct gat ctg aag ctg ggc agt	486
Leu Ser Ile Glu Gly Met Ser Ile Ser Ala Asp Leu Lys Leu Gly Ser	
110 115 120	
aac ccc acg tca ggc aag ccc acc atc acc tgc tcc agc tgc agc agc	534
Asn Pro Thr Ser Gly Lys Pro Thr Ile Thr Cys Ser Ser Cys Ser Ser	
125 130 135	
cac atc aac agt gtc cac gtg cac atc tca aag agc aaa gtc ggg tgg	582
His Ile Asn Ser Val His Val His Ile Ser Lys Ser Lys Val Gly Trp	
140 145 150	
ctg atc caa ctc ttc cac aaa aaa att gag tct gcg ctt cga aac aag	630
Leu Ile Gln Leu Phe His Lys Lys Ile Glu Ser Ala Leu Arg Asn Lys	
155 160 165	
atg aac agc cag gtc tgc gag aaa gtg acc aat tct gta tcc tcc aag	678
Met Asn Ser Gln Val Cys Glu Lys Val Thr Asn Ser Val Ser Ser Lys	
170 175 180 185	
ctg caa cct tat ttc cag act ctg cca gta atg acc aaa ata gat tct	726
Leu Gln Pro Tyr Phe Gln Thr Leu Pro Val Met Thr Lys Ile Asp Ser	
190 195 200	
gtg gct gga atc aac tat ggt ctg gtg gca cct cca gca acc acg gct	774
Val Ala Gly Ile Asn Tyr Gly Leu Val Ala Pro Pro Ala Thr Thr Ala	
205 210 215	
gag acc ctg gat gta cag atg aag ggg gag ttt tac agt gag aac cac	822
Glu Thr Leu Asp Val Gln Met Lys Gly Glu Phe Tyr Ser Glu Asn His	
220 225 230	
cac aat cca cct ccc ttt gct cca cca gtg atg gag ttt ccc gct gcc	870
His Asn Pro Pro Pro Phe Ala Pro Pro Val Met Glu Phe Pro Ala Ala	
235 240 245	
cat gac cgc atg gta tac ctg ggc ctc tca gac tac ttc ttc aac aca	918
His Asp Arg Met Val Tyr Leu Gly Leu Ser Asp Tyr Phe Phe Asn Thr	
250 255 260 265	

-3-

gcc ggg ctt gta tac caa gag gct ggg gtc ttg aag atg acc ctt aga 966
 Ala Gly Leu Val Tyr Gln Glu Ala Gly Val Leu Lys Met Thr Leu Arg
 270 275 280

gat gac atg att cca aag gag tcc aaa ttt cga ctg aca acc aag ttc 1014
 Asp Asp Met Ile Pro Lys Glu Ser Lys Phe Arg Leu Thr Thr Lys Phe
 285 290 295

ttt gga acc ttc cta cct gag gtg gcc aag aag ttt ccc aac atg aag 1062
 Phe Gly Thr Phe Leu Pro Glu Val Ala Lys Lys Phe Pro Asn Met Lys
 300 305 310

ata cag atc cat gtc tca gcc tcc acc ccg cca cac ctg tct gtg cag 1110
 Ile Gln Ile His Val Ser Ala Ser Thr Pro Pro His Leu Ser Val Gln
 315 320 325

ccc acc ggc ctt acc ttc tac cct gcc gtg gat gtc cag gcc ttt gcc 1158
 Pro Thr Gly Leu Thr Phe Tyr Pro Ala Val Asp Val Gln Ala Phe Ala
 330 335 340 345

gtc ctc ccc aac tcc tcc ctg gct tcc ctc ttc ctg att ggc atg cac 1206
 Val Leu Pro Asn Ser Ser Leu Ala Ser Leu Phe Leu Ile Gly Met His
 350 355 360

aca act ggt tcc atg gag gtc agc gcc gag tcc aac agg ctt gtt gga 1254
 Thr Thr Gly Ser Met Glu Val Ser Ala Glu Ser Asn Arg Leu Val Gly
 365 370 375

gag ctc aag ctg gat agg ctg ctc ctg gaa ctg aag cac tca aat att 1302
 Glu Leu Lys Leu Asp Arg Leu Leu Glu Leu Lys His Ser Asn Ile
 380 385 390

ggc ccc ttc ccg gtt gaa ttg ctg cag gat atc atg aac tac att gta 1350
 Gly Pro Phe Pro Val Glu Leu Leu Gln Asp Ile Met Asn Tyr Ile Val
 395 400 405

ccc att ctt gtg ctg ccc agg gtt aac gag aaa cta cag aaa ggc ttc 1398
 Pro Ile Leu Val Leu Pro Arg Val Asn Glu Lys Leu Gln Lys Gly Phe
 410 415 420 425

cct ctc ccg acg ccg gcc aga gtc cag ctc tac aac gta gtg ctt cag 1446
 Pro Leu Pro Thr Pro Ala Arg Val Gln Leu Tyr Asn Val Val Leu Gln
 430 435 440

cct cac cag aac ttc ctg ctg ttc ggt gca gac gtt gtc tat aaa 1491
 Pro His Gln Asn Phe Leu Leu Phe Gly Ala Asp Val Val Tyr Lys
 445 450 455

tgaaggcacc aggggtgccg ggggctgtca gccgcacctg ttectgatgg gctgtggggc 1551

accggctgcc ttccccagg gaatcctctc cagatcttaa ccaagagccc cttgcaaaact 1611

tcttcgactc agattcagaa atgatctaaa cacgaggaaa cattattcat tggaaaagtg 1671

catggtgtgt attttaggga ttatgagctt ctttcaaggg ctaaggctgc agagatatatt 1731

cctccaggaa tegtgtttca attgtaacca agaaatttcc atttgtgctt catgaaaaaa 1791

-4-

aacttctggt ttttttcatg tg

1813

<210> 2

<211> 487

<212> PRT

<213> Human

<223> "rBPI"

<400> 2

Met Arg Glu Asn Met Ala Arg Gly Pro Cys Asn Ala Pro Arg Trp Val
 -30 -25 -20

Ser Leu Met Val Leu Val Ala Ile Gly Thr Ala Val Thr Ala Ala Val
 -15 -10 -5 -1 1

Asn Pro Gly Val Val Val Arg Ile Ser Gln Lys Gly Leu Asp Tyr Ala
 5 10 15

Ser Gln Gln Gly Thr Ala Ala Leu Gln Lys Glu Leu Lys Arg Ile Lys
 20 25 30

Ile Pro Asp Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys Gly
 35 40 45

His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe Gln Leu Pro Ser
 50 55 60 65

Ser Gln Ile Ser Met Val Pro Asn Val Gly Leu Lys Phe Ser Ile Ser
 70 75 80

Asn Ala Asn Ile Lys Ile Ser Gly Lys Trp Lys Ala Gln Lys Arg Phe
 85 90 95

Leu Lys Met Ser Gly Asn Phe Asp Leu Ser Ile Glu Gly Met Ser Ile
 100 105 110

Ser Ala Asp Leu Lys Leu Gly Ser Asn Pro Thr Ser Gly Lys Pro Thr
 115 120 125

Ile Thr Cys Ser Ser Cys Ser Ser His Ile Asn Ser Val His Val His
 130 135 140 145

Ile Ser Lys Ser Lys Val Gly Trp Leu Ile Gln Leu Phe His Lys Lys
 150 155 160

Ile Glu Ser Ala Leu Arg Asn Lys Met Asn Ser Gln Val Cys Glu Lys
 165 170 175

Val Thr Asn Ser Val Ser Ser Lys Leu Gln Pro Tyr Phe Gln Thr Leu
 180 185 190

Pro Val Met Thr Lys Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly Leu
 195 200 205

Val Ala Pro Pro Ala Thr Thr Ala Glu Thr Leu Asp Val Gln Met Lys
 210 215 220 225

-5-

Gly Glu Phe Tyr Ser Glu Asn His His Asn Pro Pro Pro Phe Ala Pro
 230 235 240
 Pro Val Met Glu Phe Pro Ala Ala His Asp Arg Met Val Tyr Leu Gly
 245 250 255
 Leu Ser Asp Tyr Phe Phe Asn Thr Ala Gly Leu Val Tyr Gln Glu Ala
 260 265 270
 Gly Val Leu Lys Met Thr Leu Arg Asp Asp Met Ile Pro Lys Glu Ser
 275 280 285
 Lys Phe Arg Leu Thr Thr Lys Phe Phe Gly Thr Phe Leu Pro Glu Val
 290 295 300 305
 Ala Lys Lys Phe Pro Asn Met Lys Ile Gln Ile His Val Ser Ala Ser
 310 315 320
 Thr Pro Pro His Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr Pro
 325 330 335
 Ala Val Asp Val Gln Ala Phe Ala Val Leu Pro Asn Ser Ser Leu Ala
 340 345 350
 Ser Leu Phe Leu Ile Gly Met His Thr Thr Gly Ser Met Glu Val Ser
 355 360 365
 Ala Glu Ser Asn Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu Leu
 370 375 380 385
 Leu Glu Leu Lys His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu Leu
 390 395 400
 Gln Asp Ile Met Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg Val
 405 410 415
 Asn Glu Lys Leu Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg Val
 420 425 430
 Gln Leu Tyr Asn Val Val Leu Gln Pro His Gln Asn Phe Leu Leu Phe
 435 440 445
 Gly Ala Asp Val Val Tyr Lys
 450 455

<210> 3

<211> 456

<212> PRT

<213> Human

<220>

<223> bactericidal/permeability-increasing protein (BPI)
 (Figure 5)

<400> 3

FROM

(THU) 3. 27' 03 17:12 17:02/NO. 4861049210 P 33

-6-

Val Asn Pro Gly Val Val Val Arg Ile Ser Gln Lys Gly Leu Asp Tyr
 1 5 10 15
 Ala Ser Gln Gln Gly Thr Ala Ala Leu Gln Lys Glu Leu Lys Arg Ile
 20 25 30
 Lys Ile Pro Asp Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys
 35 40 45
 Gly His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe Gln Leu Pro
 50 55 60
 Ser Ser Gln Ile Ser Met Val Pro Asn Val Gly Leu Lys Phe Ser Ile
 65 70 75 80
 Ser Asn Ala Asn Ile Lys Ile Ser Gly Lys Trp Lys Ala Gln Lys Arg
 85 90 95
 Phe Leu Lys Met Ser Gly Asn Phe Asp Leu Ser Ile Glu Gly Met Ser
 100 105 110
 Ile Ser Ala Asp Leu Lys Leu Gly Ser Asn Pro Thr Ser Gly Lys Pro
 115 120 125
 Thr Ile Thr Cys Ser Ser Cys Ser Ser His Ile Asn Ser Val His Val
 130 135 140
 His Ile Ser Lys Ser Lys Val Gly Trp Leu Ile Gln Leu Phe His Lys
 145 150 155 160
 Lys Ile Glu Ser Ala Leu Arg Asn Lys Met Asn Ser Gln Val Cys Glu
 165 170 175
 Lys Val Thr Asn Ser Val Ser Ser Glu Leu Gln Pro Tyr Phe Gln Thr
 180 185 190
 Leu Pro Val Met Thr Lys Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly
 195 200 205
 Leu Val Ala Pro Pro Ala Thr Thr Ala Glu Thr Leu Asp Val Gln Met
 210 215 220
 Lys Gly Glu Phe Tyr Ser Glu Asn His His Asn Pro Pro Pro Phe Ala
 225 230 235 240
 Pro Pro Val Met Glu Phe Pro Ala Ala His Asp Arg Met Val Tyr Leu
 245 250 255
 Gly Leu Ser Asp Tyr Phe Phe Asn Thr Ala Gly Leu Val Tyr Gln Glu
 260 265 270
 Ala Gly Val Leu Lys Met Thr Leu Arg Asp Asp Met Ile Pro Lys Glu
 275 280 285
 Ser Lys Phe Arg Leu Thr Thr Lys Phe Phe Gly Thr Phe Leu Pro Glu
 290 295 300

FROM

(THU) 3. 27' 03 17:13 17:02/NO. 4861049210 P 34

-7-

Val Ala Lys Lys Phe Pro Asn Met Lys Ile Gln Ile His Val Ser Ala
305 310 315 320

Ser Thr Pro Pro His Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr
325 330 335

Pro Ala Val Asp Val Gln Ala Phe Ala Val Leu Pro Asn Ser Ser Leu
340 345 350

Ala Ser Leu Phe Leu Ile Gly Met His Thr Thr Gly Ser Met Glu Val
355 360 365

Ser Ala Glu Ser Asn Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu
370 375 380

Leu Leu Glu Leu Lys His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu
385 390 395 400

Leu Gln Asp Ile Met Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg
405 410 415

Val Asn Glu Lys Leu Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg
420 425 430

Val Gln Leu Tyr Asn Val Val Leu Gln Pro His Gln Asn Phe Leu Leu
435 440 445

Phe Gly Ala Asp Val Val Tyr Lys
450 455

<210> 4
<211> 456
<212> PRT
<213> Human

<220>
<223> lipopolysaccharide binding protein (LBP) (Figure
5)

<400> 4
Ala Asn Pro Gly Leu Val Ala Arg Ile Thr Asp Lys Gly Leu Gln Tyr
1 5 10 15

Ala Ala Gln Glu Gly Leu Leu Ala Leu Gln Ser Glu Leu Leu Arg Ile
20 25 30

Thr Leu Pro Asp Phe Thr Gly Asp Leu Arg Ile Pro His Val Gly Arg
35 40 45

Gly Arg Tyr Glu Phe His Ser Leu Asn Ile His Ser Cys Glu Leu Leu
50 55 60

His Ser Ala Leu Arg Pro Val Pro Gly Gln Gly Leu Ser Leu Ser Ile
65 70 75 80

Ser Asp Ser Ser Ile Arg Val Gln Gly Arg Trp Lys Val Arg Lys Ser
85 90 95

FROM

(THU) 3. 27' 03 17:13 17:02/NO. 4861049210 P 35

-8-

Phe Phe Lys Leu Gln Gly Ser Phe Asp Val Ser Val Lys Gly Ile Ser
 100 105 110
 Ile Ser Val Asn Leu Leu Leu Gly Ser Glu Ser Ser Gly Arg Pro Thr
 115 120 125
 Val Thr Ala Ser Ser Cys Ser Ser Asp Ile Ala Asp Val Glu Val Asp
 130 135 140
 Met Ser Gly Asp Leu Gly Trp Leu Leu Asn Leu Phe His Asn Gln Ile
 145 150 155 160
 Glu Ser Lys Phe Gln Lys Val Leu Glu Ser Arg Ile Cys Glu Met Ile
 165 170 175
 Gln Lys Ser Val Ser Ser Asp Leu Gln Pro Tyr Leu Gln Thr Leu Pro
 180 185 190
 Val Thr Thr Glu Ile Asp Ser Phe Ala Asp Ile Asp Tyr Ser Leu Val
 195 200 205
 Glu Ala Pro Arg Ala Thr Ala Gln Met Leu Glu Val Met Phe Lys Gly
 210 215 220
 Glu Ile Phe His Arg Asn His Arg Ser Pro Val Thr Leu Leu Ala Ala
 225 230 235 240
 Val Met Ser Leu Pro Glu Glu His Asn Lys Met Val Tyr Phe Ala Ile
 245 250 255
 Ser Asp Tyr Val Phe Asn Thr Ala Ser Leu Val Tyr His Glu Glu Gly
 260 265 270
 Tyr Leu Asn Phe Ser Ile Thr Asp Asp Met Ile Pro Pro Asp Ser Asn
 275 280 285
 Ile Arg Leu Thr Thr Lys Ser Phe Arg Pro Phe Val Pro Arg Leu Ala
 290 295 300
 Arg Leu Tyr Pro Asn Met Asn Leu Glu Leu Gln Gly Ser Val Pro Ser
 305 310 315 320
 Ala Pro Leu Leu Asn Phe Ser Pro Gly Asn Leu Ser Val Asp Pro Tyr
 325 330 335
 Met Glu Ile Asp Ala Phe Val Leu Leu Pro Ser Ser Ser Lys Glu Pro
 340 345 350
 Val Phe Arg Leu Ser Val Ala Thr Asn Val Ser Ala Thr Leu Thr Phe
 355 360 365
 Asn Thr Ser Lys Ile Thr Gly Phe Leu Lys Pro Gly Lys Val Lys Val
 370 375 380
 Glu Leu Lys Glu Ser Lys Val Gly Leu Phe Asn Ala Glu Leu Leu Glu
 385 390 395 400

-9-

Ala Leu Leu Asn Tyr Tyr Ile Leu Asn Thr Phe Tyr Pro Lys Phe Asn
405 410 415

Asp Lys Leu Ala Glu Gly Phe Pro Leu Pro Leu Leu Lys Arg Val Gln
420 425 430

Leu Tyr Asp Leu Gly Leu Gln Ile His Lys Asp Phe Leu Phe Leu Gly
435 440 445

Ala Asn Val Gln Tyr Met Arg Val
450 455

<210> 5
<211> 476
<212> PRT
<213> Human

<220>
<223> phospholipid transfer protein (PLTP) (Figure 5)

<400> 5
Glu Phe Pro Gly Cys Lys Ile Arg Val Thr Ser Lys Ala Leu Glu Leu
1 5 10 15

Val Lys Gln Glu Gly Leu Arg Phe Leu Glu Gln Glu Leu Glu Thr Ile
20 25 30

Thr Ile Pro Asp Leu Arg Gly Lys Glu Gly His Phe Tyr Tyr Asn Ile
35 40 45

Ser Glu Val Lys Val Thr Glu Leu Gln Leu Thr Ser Ser Glu Leu Asp
50 55 60

Phe Gln Pro Gln Gln Glu Leu Met Leu Gln Ile Thr Asn Ala Ser Leu
65 70 75 80

Gly Leu Arg Phe Arg Arg Gln Leu Leu Tyr Trp Phe Phe Tyr Asp Gly
85 90 95

Gly Tyr Ile Asn Ala Ser Ala Glu Gly Val Ser Ile Arg Thr Gly Leu
100 105 110

Glu Leu Ser Arg Asp Pro Ala Gly Arg Met Lys Val Ser Asn Val Ser
115 120 125

Cys Gln Ala Ser Val Ser Arg Met His Ala Ala Phe Gly Gly Thr Phe
130 135 140

Lys Lys Val Tyr Asp Phe Leu Ser Thr Phe Ile Thr Ser Gly Met Arg
145 150 155 160

Phe Leu Leu Asn Gln Gln Ile Cys Pro Val Leu Tyr His Ala Gly Thr
165 170 175

Val Leu Leu Asn Ser Leu Leu Asp Thr Val Pro Val Arg Ser Ser Val
180 185 190

FROM

(THU) 3. 27' 03 17:13 17:02/NO. 4861049210 P 37

-10-

Asp Glu Leu Val Gly Ile Asp Tyr Ser Leu Met Lys Asp Pro Val Ala
 195 200 205
 Ser Thr Ser Asn Leu Asp Met Asp Phe Arg Gly Ala Phe Phe Pro Leu
 210 215 220
 Thr Glu Arg Asn Trp Ser Leu Pro Asn Arg Ala Val Glu Pro Gln Leu
 225 230 235 240
 Gln Glu Glu Glu Arg Met Val Tyr Val Ala Phe Ser Glu Phe Phe Phe
 245 250 255
 Asp Ser Ala Met Glu Ser Tyr Phe Arg Ala Gly Ala Leu Gln Leu Leu
 260 265 270
 Leu Val Gly Asp Lys Val Pro His Asp Leu Asp Met Leu Leu Arg Ala
 275 280 285
 Thr Tyr Phe Gly Ser Ile Val Leu Leu Ser Pro Ala Val Ile Asp Ser
 290 295 300
 Pro Leu Lys Leu Glu Leu Arg Val Leu Ala Pro Pro Arg Cys Thr Ile
 305 310 315 320
 Lys Pro Ser Gly Thr Thr Ile Ser Val Thr Ala Ser Val Thr Ile Ala
 325 330 335
 Leu Val Pro Pro Asp Gln Pro Glu Val Gln Leu Ser Ser Met Thr Met
 340 345 350
 Asp Ala Arg Leu Ser Ala Lys Met Ala Leu Arg Gly Lys Ala Leu Arg
 355 360 365
 Thr Gln Leu Asp Leu Arg Arg Phe Arg Ile Tyr Ser Asn His Ser Ala
 370 375 380
 Leu Glu Ser Leu Ala Leu Ile Pro Leu Gln Ala Pro Leu Lys Thr Met
 385 390 395 400
 Leu Gln Ile Gly Val Met Pro Met Leu Asn Glu Arg Thr Trp Arg Gly
 405 410 415
 Val Gln Ile Pro Leu Pro Glu Gly Ile Asn Phe Val His Glu Val Val
 420 425 430
 Thr Asn His Ala Gly Phe Leu Thr Ile Gly Ala Asp Leu His Phe Ala
 435 440 445
 Lys Gly Leu Arg Glu Val Ile Glu Lys Asn Arg Pro Ala Asp Val Arg
 450 455 460
 Ala Ser Thr Ala Pro Thr Pro Ser Thr Ala Ala Val
 465 470 475

<210> 6
 <211> 470
 <212> PRT

-11-

<213> Human

<220>

<223> cholesteryl ester transfer protein (CETP) (Figure 5)

<400> 6

His	Glu	Ala	Gly	Ile	Val	Cys	Arg	Ile	Thr	Lys	Pro	Ala	Leu	Leu	Val	1	5	10	15
Leu	Asn	His	Glu	Thr	Ala	Lys	Val	Ile	Gln	Thr	Ala	Phe	Gln	Arg	Ala	20	25	30	
Ser	Tyr	Pro	Asp	Ile	Thr	Gly	Glu	Lys	Ala	Met	Met	Leu	Leu	Gly	Gln	35	40	45	
Val	Lys	Tyr	Gly	Leu	His	Asn	Ile	Gln	Ile	Ser	His	Leu	Ser	Ile	Ala	50	55	60	
Ser	Ser	Gln	Val	Glu	Leu	Val	Glu	Ala	Lys	Ser	Ile	Asp	Val	Ser	Ile	65	70	75	80
Gln	Asn	Val	Ser	Val	Val	Phe	Lys	Gly	Thr	Leu	Lys	Tyr	Gly	Tyr	Thr	85	90	95	
Thr	Ala	Trp	Trp	Leu	Gly	Ile	Asp	Gln	Ser	Ile	Asp	Phe	Glu	Ile	Asp	100	105	110	
Ser	Ala	Ile	Asp	Leu	Gln	Ile	Asn	Thr	Gln	Leu	Thr	Cys	Asp	Ser	Gly	115	120	125	
Arg	Val	Arg	Thr	Asp	Ala	Pro	Asp	Cys	Tyr	Leu	Ser	Phe	His	Lys	Leu	130	135	140	
Leu	Leu	His	Leu	Gln	Gly	Glu	Arg	Glu	Pro	Gly	Trp	Ile	Lys	Gln	Leu	145	150	155	160
Phe	Thr	Asn	Phe	Ile	Ser	Phe	Thr	Leu	Lys	Leu	Val	Leu	Lys	Gly	Gln	165	170	175	
Ile	Cys	Lys	Glu	Ile	Asn	Val	Ile	Ser	Asn	Ile	Met	Ala	Asp	Phe	Val	180	185	190	
Gln	Thr	Arg	Ala	Ala	Ser	Ile	Leu	Ser	Asp	Gly	Asp	Ile	Gly	Val	Asp	195	200	205	
Ile	Ser	Leu	Thr	Gly	Asp	Pro	Val	Ile	Thr	Ala	Ser	Tyr	Leu	Glu	Ser	210	215	220	
His	His	Lys	Gly	His	Phe	Ile	Tyr	Lys	Asn	Val	Ser	Glu	Asp	Leu	Pro	225	230	235	240
Leu	Pro	Thr	Phe	Ser	Pro	Thr	Leu	Leu	Gly	Asp	Ser	Arg	Met	Leu	Tyr	245	250	255	
Phe	Trp	Phe	Ser	Glu	Arg	Val	Phe	His	Ser	Leu	Ala	Lys	Val	Ala	Phe	260	265	270	

FROM

(THU) 3. 27' 03 17:14 17:02/NO. 4861049210 P 39

-12-

Gln Asp Gly Arg Leu Met Leu Ser Leu Met Gly Asp Glu Phe Lys Ala
275 280 285

Val Leu Glu Thr Trp Gly Phe Asn Thr Asn Gln Glu Ile Phe Gln Glu
290 295 300

Val Val Gly Gly Phe Pro Ser Gln Ala Gln Val Thr Val His Cys Leu
305 310 315 320

Lys Met Pro Lys Ile Ser Cys Gln Asn Lys Gly Val Val Val Asn Ser
325 330 335

Ser Val Met Val Lys Phe Leu Phe Pro Arg Pro Asp Gln Gln His Ser
340 345 350

Val Ala Tyr Thr Phe Glu Glu Asp Ile Val Thr Thr Val Gln Ala Ser
355 360 365

Tyr Ser Lys Lys Lys Leu Phe Leu Ser Leu Leu Asp Phe Gln Ile Thr
370 375 380

Pro Lys Thr Val Ser Asn Leu Thr Glu Ser Ser Ser Glu Ser Ile Gln
385 390 395 400

Ser Phe Leu Gln Ser Met Ile Thr Ala Val Gly Ile Pro Glu Val Met
405 410 415

Ser Arg Leu Glu Val Val Phe Thr Ala Leu Met Asn Ser Lys Gly Val
420 425 430

Ser Leu Phe Asp Ile Ile Asn Pro Glu Ile Ile Thr Arg Asp Gly Phe
435 440 445

Leu Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His Leu Leu Val Asp
450 455 460

Phe Leu Gln Ser Leu Ser
465 470

<210> 7

<211> 24

<212> DNA

<213> Human

<220>

<223> BPI-53

<400> 7

actgggtcca tggaggtcag cgcc

24

<210> 8

<211> 29

<212> DNA

<213> Human

<220>

-13-

<223> BPI-54

<400> 8

gacagatctc tcgagtcatt tatagacaa

29

<210> 9

<211> 42

<212> DNA

<213> Human

<220>

<223> oligonucleotide from XcmI site to SphI site within
BPI gene (encoding residues 348-361) containing
the codon TCC for the serine at amino acid
position 351

<400> 9

cccaactcct cccctggcttc cctcttctcg attggcatgc ac

42

<210> 10

<211> 42

<212> DNA

<213> Human

<220>

<223> Oligonucleotide complementary to SEQ ID NO:5

<400> 10

gggttcagga gggaccgaag ggagaaggac taaccgtacg tg

42

<210> 11

<211> 14

<212> PRT

<213> Human

<220>

<223> "wild type" amino acid sequence of residues
348-361 in BPI

<400> 11

Pro Asn Ser Ser Leu Ala Ser Leu Phe Leu Ile Gly Met His
1 5 10

<210> 12

<211> 42

<212> DNA

<213> Human

<220>

<223> oligonucleotide from XcmI site to SphI site within
the BPI gene (encoding residues 348-361)
containing the codon GCC for alanine at amino acid
position 351

FROM

(THU) 3. 27' 03 17:14 17:02/NO. 4861049210 P 41

-14-

<400> 12
cccaactcgc ccctggttc cctcttctg attggcatgc ac

42

<210> 13
<211> 42
<212> DNA
<213> Human

<220>
<223> Oligonucleotide complementary to SEO ID NO:8

<400> 13
gggttcaggc gggaccgaag ggagaaggac taaccgtacg tg

42

<210> 14
<211> 14
<212> PRT
<213> Human

<220>
<223> "nonglycosylated" amino acid sequence of residues
348-361 in BPI

<400> 14
Pro Asn Ser Ala Leu Ala Ser Leu Phe Leu Ile Gly Met His
1 5 10